

SEQUENCE LISTING

1. GENERAL INFORMATION:

(i) APPLICANT: Glorchen, Laurie H. et al.

(ii) TITLE OF INVENTION: Human c-Maf Compositions and
Methods of Use Thereof

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD, LLP

(B) STREET: 28 State Street

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/030,579

(B) FILING DATE: 2-FEB-1998

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Kara, Catherine J.

(B) REGISTRATION NUMBER: 41,106

(C) REFERENCE/DOCKET NUMBER: HUI-027CP

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1203 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

A NAME KEY: YES
B IDENTIFICATION: 1111213

5 81 SEQUENCE DESCRIPTION: SEQ ID: 111

ATG GAA TTA GAA TTA GAA ATG AAT AAT TTT GAT CTG GAT AAT AAT TTT
48
Met Ala Ser Ile Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
10 1 5 10 15

TTG GGC ATG GAA TAT GTT AAT GAC TTC TAT TTG ATG AAG TTT GAA TTG
76
Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
15 20 25 30

AAA AAG GAA CCG GTG GAG ACC GAC GGC ATC ATC AGC CAG TGC GAT CTT
144
Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
20 35 40 45

CTC ATC GCC GGG GGC TCG CTG TCC TCC ACC CCC ATG AGC ACC CCC TAT
192
Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
25 50 55 60

AGC TCG GTG CCC CCG TCC CCC AGC TTC TCG GCG CCC AGC CCG GGC TCG
240
Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
30 65 70 75 80

CGA GGC GAA CAG AAG GCG CAC CTG GAA GAC TAC TAC TGG ATG ACC GGC
288
Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
35 85 90 95

TAC CCG CAG CAG CTG AAC CCC GAG GCG CTG GGC TTC AGC CCC GAG GAC
336
Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
40 100 105 110

GCG GTC GAG GCG CTC ATC AGC AAC AGC CAC CAG CTC CGG GGC GGC TTC
384
Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe
45 115 120 125

GAT GGC TAT GCG CGC GGG GCG CAG CAG CTA GCC GCG GCG GCC GGG GCA
432
Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Ala Gly Ala
50 130 135 140

GGT GCC GGC GCC TCC TTG GGC GGC AGC GGC GAG GAG ATG GGC CCC GCC
480
Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala
55 145 150 155 160

123 GGT TTA TTS TCG GAT GTG ATA TAC TAT TCG GGT TAT CAG AGC GTC
 124
 Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala His Ser Gly
 175 176 177
 5
 178 GGT TTA TAC TAC CAC CAC CAC CAC CAC CAC GGT TTA TAT CAC CAC
 179
 Ala Gly His His Tyr His His His His His His Ala Ala Gly His His
 180 181 182 183 184 185 186 187 188 189 190
 10
 CAC CAC CCG ACG GCC GGC GCG CCC GGC GCC GCG GGC AGC GCG GCC GGT
 191
 His His His Thr Ala Gly Ala His Gly Ala Ala Gly Ser Ala Ala Ala
 192 193 194 195 196 197 198 199 200 201 202 203
 15
 TCG GCC GGT GGC GGT GGG GGC GCG GGC GGC GGT GGC CCG GCC AGC GTT
 204
 Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly His Ala Ser Val
 210 211 212 213 214 215 216 217 218 219 220
 20
 GGG GGC GGC GGC GGC GGC GGC GGC GGC GGA GGC GGC GGC GGC GGC GGC
 221
 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala
 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240
 25
 GGC GCC CTG CAC CCG CAC CAC GCC GCC GGC GGC CTG CAC TTC GAC GAC
 241
 Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp
 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260
 30
 CGC TTC TCC GAC GAG CAG CTG GTG ACC ATG TCT GTG CGC GAC TGG AAC
 261
 Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn
 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280
 35
 CGG CAG CTG CGC GGG GTC AGC AAG GAG GAG GTG ATC CGG CTG AAG CAG
 281
 Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln
 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300
 40
 AAG AGG CCG ACC CTG AAA AAC CGC GGC TAT GCC AAG TCC TGC CGC TTC
 301
 Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe
 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320
 45
 AAG AGG GTG CAG CAG AGA CAC GTC CTG GAG TCG GAG AAG AAC CAG CTG
 321
 Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu
 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340
 50
 CTG CAG CAA GTC GAC CAC CTC AAG CAG GAG ATC TCC AGG CTG GTG CGC
 341
 Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg
 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360
 55
 GAG AGG GAC GCG TAC AAG GAG AAA TAC GAG AAG TTG GTG AGC AGC GGC
 361
 1056

110 Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly
340 345 350

5 TTC GGA GAA AAC GGC TCG AGC AGC GAC AAC CCG TCG TCT CCC GAG TTT
1104
110 Arg Gln Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Gln Phe
355 360 365

10 TTC ATA ACT GAG CCC ACT CGC AAG TTG GAG CCA TCA GTG GGA TAC GCC
1152
Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala
370 375 380

15 ACA TTT TGG AAG CCC CAG CAT CGT GTA CTT ACC AGT GTG TTC ACA AAA
1200
Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys
385 390 395 400

20 TGA
1203

25 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 amino acids
(B) TYPE: amino acid
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ser Glu Leu Ala Met Ser Asn Ser Asp Leu Pro Thr Ser Pro
1 5 10 15

Leu Ala Met Glu Tyr Val Asn Asp Phe Asp Leu Met Lys Phe Glu Val
40 20 25 30

Lys Lys Glu Pro Val Glu Thr Asp Arg Ile Ile Ser Gln Cys Gly Arg
35 40 45

45 Leu Ile Ala Gly Gly Ser Leu Ser Ser Thr Pro Met Ser Thr Pro Cys
50 55 60

Ser Ser Val Pro Pro Ser Pro Ser Phe Ser Ala Pro Ser Pro Gly Ser
65 70 75 80

5 Arg Gly Glu Gln Lys Ala His Leu Glu Asp Tyr Tyr Trp Met Thr Gly
85 90 95

55 Tyr Pro Gln Gln Leu Asn Pro Glu Ala Leu Gly Phe Ser Pro Glu Asp
100 105 110

Ala Val Glu Ala Leu Ile Ser Asn Ser His Gln Leu Arg Gly Gly Phe

	115	120	125
	Asp Gly Tyr Ala Arg Gly Ala Gln Gln Leu Ala Ala Ala Gly Ala		
	130	135	140
5	Gly Ala Gly Ala Ser Leu Gly Gly Ser Gly Glu Glu Met Gly Pro Ala		
	145	150	155 160
	Ala Ala Val Val Ser Ala Val Ile Ala Ala Ala Ala Ala Gln Ser Gly		
10		165	170 175
	Ala Gly Pro His Tyr His His His His His His Ala Ala Gly His His		
	180	185	190
15	His His Pro Thr Ala Gly Ala Pro Gly Ala Ala Gly Ser Ala Ala Ala		
	195	200	205
	Ser Ala Gly Gly Ala Gly Gly Ala Gly Gly Gly Gly Gly Pro Ala Ser Val		
20	210	215	220
	Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Ala Ala		
	225	230	235 240
	Gly Ala Leu His Pro His His Ala Ala Gly Gly Leu His Phe Asp Asp		
25		245	250 255
	Arg Phe Ser Asp Glu Gln Leu Val Thr Met Ser Val Arg Asp Trp Asn		
	260	265	270
30	Arg Gln Leu Arg Gly Val Ser Lys Glu Glu Val Ile Arg Leu Lys Gln		
	275	280	285
	Lys Arg Arg Thr Leu Lys Asn Arg Gly Tyr Ala Lys Ser Cys Arg Phe		
35	290	295	300
	Lys Arg Val Gln Gln Arg His Val Leu Glu Ser Glu Lys Asn Gln Leu		
	305	310	315 320
	Leu Gln Gln Val Asp His Leu Lys Gln Glu Ile Ser Arg Leu Val Arg		
40		325	330 335
	Glu Arg Asp Ala Tyr Lys Glu Lys Tyr Glu Lys Leu Val Ser Ser Gly		
	340	345	350
45	Phe Arg Glu Asn Gly Ser Ser Ser Asp Asn Pro Ser Ser Pro Glu Phe		
	355	360	365
	Phe Ile Thr Glu Pro Thr Arg Lys Leu Glu Pro Ser Val Gly Tyr Ala		
50	370	375	380
	Thr Phe Trp Lys Pro Gln His Arg Val Leu Thr Ser Val Phe Thr Lys		
	385	390	395 400